Noncompartmental vs. Compartmental Approaches to Pharmacokinetic Data Analysis

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## Questions To Be Asked

## > Pharmacokinetics

- What the body does to the drug
> Pharmacodynamics
- What the drug does to the body
> Disease progression
- Measurable therapeutic effect
> Variability
- Sources of error and biological variation


## Pharmacokinetics / Pharmacodynamics

```
> Pharmacokinetics > Pharmacodynamics
>"What the body does to > "What the drug does to
    the drug"
> Fairly well known > Largely unknown
 Useful to get to the PD > Has clinical relevance
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## Pharmacokinetic Parameters

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> Definition of pharmacokinetic parameters $\qquad$

- Descriptive or observational
- Quantitative (requiring a formula and a means
$\qquad$ to estimate using the formula)
$>$ Formulas for the pharmacokinetic parameters
> Methods to estimate the parameters from the formulas using measured data
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## Goals Of This Lecture

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Description of the parameters of interest
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> Underlying assumptions of noncompartmental and compartmental models
> Parameter estimation methods
$>$ What to expect from the analysis
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## Goals Of This Lecture

$>$ What this lecture is about

- What are the assumptions, and how can these affect the conclusions
- Make an intelligent choice of methods depending upon what information is required $\qquad$ from the data
$>$ What this lecture is not about $\qquad$
- To conclude that one method is "better" than another


## A Drug In The Body: Constantly Undergoing Change

$>$ Absorption
> Transport in the circulation
> Transport across membranes
> Biochemical transformation
> Elimination
$\rightarrow$ ADME

- Absorption, Distribution, Metabolism, Excretion



## Kinetics <br> And Pharmacokinetics

Kinetics

- The temporal and spatial distribution of a substance in a system.
> Pharmacokinetics
- The temporal and spatial distribution of a drug (or drugs) in a system.


A Drug In The Body:
Constantly Undergoing Change


A Drug In The Body:
Constantly Undergoing Change

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## Spatially Distributed Models

$>$ Spatially realistic models:

- Require a knowledge of physical chemistry, irreversible thermodynamics and circulatory dynamics.
- Are difficult to solve.
- It is difficult to design an experiment to estimate their parameter values.
$>$ While desirable, normally not practical.
$>$ Question: What can one do?


## Resolving The Problem

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Reducing the system to a finite number of $\qquad$ components
> Lumping processes together based upon time, location or a combination of the two
> Space is not taken directly into account: rather, spatial heterogeneity is modeled through changes that occur in time

## Lumped Parameter Models

$>$ Models which make the system discrete $\qquad$ through a lumping process thus eliminating the need to deal with partial differential equations.
> Classes of such models: $\qquad$

- Noncompartmental models
- Based on algebraic equations
- Compartmental models
- Based on linear or nonlinear differential equations


## Probing The System

> Accessible pools: These are system spaces that are available to the experimentalist for test input and/or measurement.
> Nonaccessible pools:
These are spaces comprising the rest of the system which are not available for test input and/or measurement.

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## Focus On The Accessible Pool

$\qquad$ INPUT SOURCE MEASURE $\qquad$
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## Characteristics Of The Accessible Pool

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$\qquad$
Kinetically Homogeneous
Instantaneously Well-mixed

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## The Pharmacokinetic Parameters

$>$ Which pharmacokinetic parameters can we estimate based on measurements in the accessible pool?
> Estimation requires a model

- Conceptualization of how the system works
> Depending on assumptions:
- Noncompartmental approaches
- Compartmental approaches

Accessible Pool \& System
Assumptions $\rightarrow$ Information
> Accessible pool

- Initial volume of distribution
- Clearance rate
- Elimination rate constant
- Mean residence time
> System
- Equivalent volume of distribution
- System mean residence time
- Bioavailability
- Absorption rate constant


## Compartmental and Noncompartmental Analysis

The only difference between the two methods is in how the nonaccessible portion of the system is described
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## The Noncompartmental Model


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## Single Accessible Pool

 Noncompartmental Model$>$ Parameters (IV bolus and infusion)

- Mean residence time
- Clearance rate
- Volume of distribution
$>$ Estimating the parameters from data
> Additional assumption:
- Constancy of kinetic distribution parameters


## Mean Residence Time

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$>$ The average time that a molecule of drug $\qquad$ spends in the system

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## Areas Under The Curve

> AUMC

- Area Under the Moment Curve
> AUC
- Area Under the Curve
> MRT $\qquad$
- "Normalized" AUMC (units = time)

$$
\mathrm{MRT}=\frac{\int_{0}^{+\infty} \mathrm{C}(\mathrm{t}) \mathrm{dt}}{\int_{0}^{+\infty} \mathrm{C}(\mathrm{t}) \mathrm{dt}}=\frac{\mathrm{AUMC}}{\mathrm{AUC}}
$$

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## What Is Needed For MRT?

> Estimates for AUC and AUMC.

$$
A U C=\int_{0}^{\infty} C(t) d t=\int_{0}^{t_{1}} C(t) d t+\int_{t_{1}}^{t_{n}} C(t) d t+\int_{t_{n}}^{\infty} C(t) d t
$$

$\mathrm{A} U M \mathrm{C}=\int_{0}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}=\int_{0}^{\mathrm{t}_{1}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{1}}^{\mathrm{t}_{\mathrm{n}}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}$
> They require extrapolations beyond the time frame of the experiment
$>$ Thus, this method is not model independent as often claimed.

$$
\begin{gathered}
\text { Estimating AUC And AUMC Using } \\
\text { Sums Of Exponentials } \\
\text { AUC }=\int_{0}^{\infty} C(t) d t=\int_{0}^{t_{0}^{1}} C(t) d t+\int_{t_{1}}^{t^{h} C(t) d t+\int_{h_{n}}^{\infty} C(t) d t} \\
\text { AUMC }=\int_{0}^{\infty} \cdot C(t) d t=\int_{0}^{t_{0}^{1} t \cdot C(t) d t+\int_{t_{1}}^{t_{1}} t \cdot C(t) d t+\int_{t_{n}}^{x} t \cdot C(t) d t} \\
C(t)=A_{1} e^{-\lambda_{1} t}+\cdots+A_{n} e^{-\lambda_{n} t}
\end{gathered}
$$

| What Is Needed For MRT? |
| :--- |
| $>$ Estimates for AUC and AUMC. |
| AUC $=\int_{0}^{\infty} \mathrm{C}(t) d t=\int_{0}^{t_{1}} \mathrm{C}(t) d t+\int_{t_{1}}^{t_{n}} \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{t_{n}}^{\infty} \mathrm{C}(t) d t$ |
| AUMC $=\int_{0}^{\infty} \cdot \mathrm{C}\left(\mathrm{C}(\mathrm{t}) \mathrm{dt}=\int_{0}^{t_{1}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{1}}^{t_{n}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}\right.$ |
| $>$ They require extrapolations beyond the time |
| frame of the experiment |
| $>$ Thus, this method is not model independent as |
| often claimed. |

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Bolus IV Injection
Formulas can be extended to other administration modes

$$
\begin{gathered}
A \cup C=\int_{0}^{\infty} C(t) d t=\frac{A_{1}}{\lambda_{1}}+\cdots+\frac{A_{n}}{\lambda_{n}} \\
A U M C=\int_{0}^{\infty} t \cdot C(t) d t=\frac{A_{1}}{\lambda_{1}^{2}}+\cdots+\frac{A_{n}}{\lambda_{n}^{2}} \\
C(0)=A_{1}+\cdots+A_{n}
\end{gathered}
$$

## The Integrals

> These other methods provide formulas for $\qquad$ the integrals between $t_{1}$ and $t_{n}$ leaving it up to the researcher to extrapolate to time zero and time infinity.

$$
A U C=\int_{0}^{\infty} C(t) d t=\int_{0}^{t_{1}} C(t) d t+\int_{t_{1}}^{t_{n}} C(t) d t+\int_{t_{n}}^{\infty} C(t) d t
$$

$\mathrm{A} U M C=\int_{0}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}=\int_{0}^{\mathrm{t}_{1}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{1}}^{\mathrm{t}_{\mathrm{n}}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}$
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| The Integrals |
| :---: |
| $>$ These other methods provide formulas for |
| the integrals between $t_{1}$ and $t_{n}$ leaving it up |
| to the researcher to extrapolate to time |
| zero and time infinity. |
| AUC $=\int_{0}^{\infty} \mathrm{C}(\mathrm{t}) \mathrm{dt}=\int_{0}^{\mathrm{t}_{1}} \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{1}}^{t_{n}} \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{n}}^{\infty} \mathrm{C}(\mathrm{t}) \mathrm{dt}$ |
| $\mathrm{AUMC}=\int_{0}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}=\int_{0}^{t_{1}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{1}}^{\mathrm{t}_{n}} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}+\int_{\mathrm{t}_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}$ |

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## Trapezoidal Rule

$>$ For every time $t_{i}, i=1, \ldots, n$ $A \cup C_{i-1}^{i}=\frac{1}{2}\left[y_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}}\right)+\mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}-1}\right)\right]\left(\mathrm{t}_{\mathrm{i}}-\mathrm{t}_{\mathrm{i}-1}\right)$
AUMC $_{\mathrm{i}-1}^{\mathrm{i}}=\frac{1}{2}\left[\mathrm{t}_{\mathrm{i}} \cdot \mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}}\right)+\mathrm{t}_{\mathrm{i}-1} \cdot \mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}-1}\right)\right]\left(\mathrm{t}_{\mathrm{i}}-\mathrm{t}_{\mathrm{i}-1}\right)$

$\qquad$
$t_{i-1} t_{i}$

## Log-trapezoidal Rule

$\qquad$
$>$ For every time $\mathrm{t}_{\mathrm{i}}, \mathrm{i}=1, \ldots, \mathrm{n}$ $\qquad$
$\operatorname{AUC}_{i-1}^{i}=\frac{1}{\ln \left(\frac{y_{\text {obs }}\left(t_{i}\right)}{y_{\text {obs }}\left(t_{i-1}\right)}\right)}\left[y_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}}\right)+\mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}-1}\right)\right]\left(\mathrm{t}_{\mathrm{i}}-\mathrm{t}_{\mathrm{i}-1}\right)$
$\operatorname{AUMC}_{\mathrm{i}-1}^{i}=\frac{1}{\ln \left(\frac{\mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}}\right)}{\mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}-1}\right)}\right)}\left[\mathrm{t}_{\mathrm{i}} \cdot y_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}}\right)+\mathrm{t}_{\mathrm{i}-1} \mathrm{y}_{\text {obs }}\left(\mathrm{t}_{\mathrm{i}-1}\right)\right]\left(\mathrm{t}_{\mathrm{i}}-\mathrm{t}_{\mathrm{i}-1}\right)$

Trapezoidal Rule Potential Pitfalls

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As the number of samples decreases, the $\qquad$ interpolation may not be accurate (depends on the shape of the curve)
> Extrapolation from last measurement necessary
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## Extrapolating From $\mathrm{t}_{\mathrm{n}}$ To Infinity

$>$ Terminal decay is assumed to be a monoexponential
$>$ The corresponding exponent is often called $\lambda_{z}$.
$>$ Half-life of terminal decay can be calculated:
$t_{z / 1 / 2}=\ln (2) / \lambda_{z}$

## Extrapolating From $\mathrm{t}_{\mathrm{n}}$ To Infinity

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From last data point:
$\qquad$
$A \cup C_{\text {extrap -dat }}=\int_{t_{n}}^{\infty} C(t) d t=\frac{y_{\text {oos }}\left(t_{n}\right)}{\lambda_{z}}$
$\mathrm{AUMC}_{\text {extrap-dat }}=\int_{\mathrm{t}_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}=\frac{\mathrm{t}_{\mathrm{n}} \cdot \cdot_{\text {obss }}\left(\mathrm{t}_{n}\right)}{\lambda_{z}}+\frac{y_{\text {obs }}\left(\mathrm{t}_{\mathrm{n}}\right)}{\lambda_{z}^{2}}$
$\qquad$

From last calculated value:

$$
\begin{gathered}
A U C_{\text {extrap-calc }}=\int_{t_{n}}^{\infty} C(t) d t=\frac{A_{2} e^{-\lambda_{2} t_{n}}}{\lambda_{2}} \\
A U M C_{\text {extap-calc }}=\int_{t_{n}}^{\infty} \mathrm{t} \cdot \mathrm{C}(\mathrm{t}) \mathrm{dt}=\frac{\mathrm{t}_{\mathrm{n}} \cdot \mathrm{~A}_{2} \mathrm{e}^{-\lambda_{2} t_{n}}}{\lambda_{z}}+\frac{\mathrm{A}_{2} \mathrm{e}^{-\lambda \lambda_{2} t_{n}}}{\lambda_{z}^{2}}
\end{gathered}
$$

## Extrapolating From $\mathrm{t}_{\mathrm{n}}$ To Infinity

Extrapolating function crucial $\qquad$

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## Estimating The Integrals

> To estimate the integrals, one sums up the individual components.

$A U C=\int_{0}^{\infty} C(t) d t=\int_{0}^{t_{1}} C(t) d t+\int_{t_{1}}^{t_{n}} C(t) d t+\int_{t_{n}}^{\infty} C(t) d t$<br>$A U M C=\int_{0}^{\infty} t \cdot C(t) d t=\int_{0}^{t_{1}} t \cdot C(t) d t+\int_{t_{1}}^{t_{n}} t \cdot C(t) d t+\int_{t_{n}}^{\infty} t \cdot C(t) d t$

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## Advantages Of Using Function Extrapolation (Exponentials)

> Extrapolation is automatically done as part of the data fitting
> Statistical information for all parameters (e.g. their standard errors) calculated
$>$ There is a natural connection with the solution of linear, constant coefficient compartmental models
> Software is available

## Clearance Rate

> The volume of blood cleared per unit time, $\qquad$ relative to the drug

$$
\mathrm{CL}=\frac{\text { Elimination rate }}{\text { Concentration in blood }}
$$

It can be shown that

$$
\mathrm{CL}=\frac{\text { DrugDose }}{\text { AUC }}
$$

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## Single Accessible Pool Models

$\qquad$
> Noncompartmental
> Compartmental



A Model Of The System

## Compartmental Model

> Compartment

- Instantaneously well-mixed
- Kinetically homogeneous
> Compartmental model
- Finite number of compartments
- Specifically connected
- Specific input and output


| Compartmental Model |
| :---: |
| > Compartment |
| - Instantaneously well-mixed |
| - Kinetically homogeneous |
| > Compartmental model |
| - Finite number of compartments |
| - Specifically connected |
| - Specific input and output |
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## Kinetics And The Compartmental Model

$>$ Time and space
$\frac{\partial}{\partial \mathbf{x}}, \frac{\partial}{\partial y}, \frac{\partial}{\partial z}, \frac{\partial}{\partial t}$
$\rightarrow X(x, y, z, t)$
$\rightarrow \frac{\partial X(x, y, z, t)}{\partial x}, \frac{\partial X(x, y, z, t)}{\partial y}, \frac{\partial X(x, y, z, t)}{\partial z}, \frac{\partial X(x, y, z, t)}{\partial t}$
> Time
$\frac{\mathrm{d}}{\mathrm{dt}} \rightarrow \mathrm{X}(\mathrm{t}) \rightarrow \frac{\mathrm{dX}(\mathrm{t})}{\mathrm{dt}}$

## Demystifying Differential

## Equations

It is all about modeling rates of change, i.e. slopes, or derivatives:

Rates of change may be constant or not

## Ingredients Of Model Building

$>$ Model of the system

- Independent of experiment design
- Principal components of the biological system
> Experimental design
- Two parts:
- Input function (dose, shape, protocol)
- Measurement function (sampling, location)

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Single Compartment Model
> The rate of change of the amount in the
 compartment, $\mathrm{q}_{1}(\mathrm{t})$, is equal to what enters the compartment (inputs or initial conditions), minus what leaves the compartment, a quantity proportional to

$$
\frac{\mathrm{dq}_{1}(\mathrm{t})}{\mathrm{dt}}=-\mathrm{k}(0,1) \mathrm{q}_{1}(\mathrm{t}) \quad \begin{aligned}
& \mathrm{q}_{1}(\mathrm{t}) \\
& >\mathrm{k}(0,1) \text { is a rate constant }
\end{aligned}
$$

$\qquad$
> The rate of change of the amount in the
 compartment, $q_{1}(t)$, is equal to what enters the compartment (Dose), minus what leaves the compartment, a quantity proportional to $q(t)$
$\frac{d q_{1}(t)}{d t}=-k(0,1) q_{1}(t)+\operatorname{Dose}(t)$ Dose(t) can be any function of time
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## Experiment Design <br> Modeling Input Sites

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| Experiment Design Modeling Measurement Sites |  |
| :---: | :---: |
|  | > The measurement (sample) s1 does not subtract mass or perturb the system |
|  | > The measurement equation $s 1$ links $q_{1}$ with the experiment, thus preserving the units of differential equations and data (e.g. $q_{1}$ is mass, the measurement is concentration |
| $s_{1}(t)=\frac{q_{1}(t)}{V}$ | $\begin{aligned} & \overline{\Rightarrow \mathrm{ss} 1=q_{1} N} \\ & >V=\text { volume of distribution of } \\ & \text { compartment } 1 \end{aligned}$ |

## Notation

- The fluxes $\mathrm{F}_{\mathrm{ij}(\text { from j to } i \text { ) }}$ describe material transport in units of mass per unit time

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## The Compartmental Fluxes ( $\mathrm{F}_{\mathrm{ij}}$ )

$>$ Describe movement among, into or out of
$\qquad$ a compartment
$>$ A composite of metabolic activity

- transport
- biochemical transformation
- both
>Similar (compatible) time frame
A Proportional Model For The
Compartmental Fluxes
$>\mathrm{q}=$ compartmental masses
$>\mathrm{p}=$ (unknown) system parameters
$>\mathrm{k}_{\mathrm{ji}}=\mathrm{a}$ (nonlinear) function specific to the
transfer from i to j
$\mathrm{F}_{\mathrm{ji}}(\mathrm{q}, \mathrm{p}, \mathrm{t})=\mathrm{k}_{\mathrm{ji}}(\mathrm{q}, \mathrm{p}, \mathrm{t}) \cdot \mathrm{q}_{\mathrm{i}}(\mathrm{t})$
(ref: see Jacquez and Simon)


## Nonlinear Kinetics Example

Remember the one-compartment model:

$$
\begin{aligned}
& \frac{d q 1(t)}{d t}=-k(0,1) q 1(t)+\operatorname{Dose}(t) \\
& s 1(t)=\frac{q 1(t)}{V}
\end{aligned}
$$

$>$ What if we had a concentrationdependent drug elimination rate?

## Nonlinear Kinetics: <br> Michaelis-Menten

> Michaelis-Menten kinetics:

$$
\begin{aligned}
& \frac{d q 1(t)}{d t}=-\frac{V m}{K m+c(t)} q 1(t)+\operatorname{Dose}(t) \\
& s 1(t)=\frac{q 1(t)}{V}
\end{aligned}
$$

$>$ Vm $=$ maximal metabolic rate
$>$ Km $=$ Michaelis-Menten constant

## Linear vs. Nonlinear Kinetics

$>$ If $\mathrm{Km} \gg \mathrm{c}(\mathrm{t})$ then:

$$
\begin{aligned}
& \frac{d q 1(t)}{d t} \cong-\frac{V m}{K m} q 1(t)+\operatorname{Dose}(t) \\
& s 1(t)=\frac{q 1(t)}{V}
\end{aligned}
$$

$>$ The concentration declines at a rate proportional to it (first-order kinetics)
> This is true at low concentrations (w.r.t. Km)


## Tracking Nonlinearities

> How to find nonlinear behavior?

$$
\begin{aligned}
& \frac{d q 1(t)}{d t}=-\frac{V m}{K m+c(t)} q 1(t)+\operatorname{Dose}(t) \\
& s 1(t)=\frac{q 1(t)}{V}
\end{aligned}
$$

Watch: Simulated concentration time profile for $\mathrm{D}=180 \mathrm{mg}, \mathrm{Vm}=20$ $\mathrm{mg} / \mathrm{L} / \mathrm{hr}, \mathrm{Km}=1 \mathrm{mg} / \mathrm{L}, \mathrm{v} 1=5 \mathrm{~L}$


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## The Fractional Coefficients ( $\mathrm{k}_{\mathrm{ij}}$ )

- The fractional coefficients $\mathrm{k}_{\mathrm{ij}}$ are called $\qquad$ fractional transfer functions
- If $\mathrm{k}_{\mathrm{ij}}$ does not depend on the compartmental masses, then the kij is called a fractional transfer (or rate) constant.

$$
k_{i j}(q, p, t)=k_{i j}
$$

## Compartmental Models And Systems Of Ordinary Differential Equations

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$>$ Good mixing

- permits writing $q_{i}(t)$ for the $i^{i \text { th }}$ compartment.
$>$ Kinetic homogeneity $\qquad$
- permits connecting compartments via the $\mathrm{k}_{\mathrm{ij}}$. $\qquad$
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## Linear, Constant Coefficient <br> Compartmental Models

$>$ All transfer rates $\mathrm{k}_{\mathrm{ij}}$ are constant.

- This facilitates the required computations greatly
Assume "steady state" conditions.
- Changes in compartmental mass do not affect
the values for the transfer rates
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## The $\mathrm{i}^{\text {th }}$ Compartment


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The Compartmental Matrix

$$
\begin{gathered}
\mathrm{k}_{\mathrm{ii}}=-\left(\sum_{\substack{\mathrm{j}=0 \\
j=1}}^{\mathrm{n}} \mathrm{k}_{\mathrm{ji}}\right) \\
\mathrm{K}=\left[\begin{array}{cccc}
\mathrm{k}_{11} & \mathrm{k}_{12} & \cdots & \mathrm{k}_{11} \\
\mathrm{k}_{21} & \mathrm{k}_{22} & \cdots & \mathrm{k}_{2 n} \\
\vdots & \vdots & \ddots & \vdots \\
\mathrm{k}_{\mathrm{n} 1} & \mathrm{k}_{\mathrm{n} 2} & \cdots & \mathrm{k}_{\mathrm{nn}}
\end{array}\right]
\end{gathered}
$$

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## Compartmental Model

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> A detailed postulation of how one believes a system functions.
$>$ The need to perform the same experiment
$\qquad$ on the model as one did in the laboratory.


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## Experiments

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> Need to recreate the laboratory $\qquad$ experiment on the model.
Need to specify input and measurements
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Key: UNITS

- Input usually in mass, or mass/time
- Measurement usually concentration $\qquad$
- Mass per unit volume

$\qquad$



## Parameter Estimates

$>$ Principles of model building $\qquad$

- Model definition: structure, error model
- Model selection: parsimony criteria $\qquad$
- Estimation methods: maximum likelihood
$>$ Model parameters: $\mathrm{k}_{\mathrm{ij}}$ and volumes
> Pharmacokinetic parameters: volumes, clearance, residence times, etc.
$>$ Reparameterization - changing the parameters from $k_{i j}$ to the PK parameters.


## Recovering The PK Parameters From Compartmental Models

Parameters can be based upon

- The model primary parameters
- Differential equation parameters
- Measurement parameters
- The compartmental matrix
- Aggregates of model parameters


## Compartmental Model $\Rightarrow$

 Exponential$$
\begin{aligned}
& \frac{d q_{1}(t)}{d t}=-k(0,1) q_{1}(t)+\operatorname{Dose} \delta(t) \\
& s 1(t)=\frac{q_{1}(t)}{V}
\end{aligned}
$$

For a pulse input $\delta(\mathrm{t})$
$q_{1}(t)=$ Dose $\cdot e^{-k(0,1) t}$
$s 1(t)=\frac{q_{1}(t)}{V}=\frac{\text { Dose }}{V} e^{-k(0,1) t}$
$C L=k(0,1) \times V$

## Compartmental Residence Times



Rate constants
Residence times
Intercompartmental clearances

## Parameters Based Upon The Compartmental Matrix

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$\qquad$
$\qquad$

$$
K=\left[\begin{array}{cccc}
k_{11} & k_{12} & \cdots & k_{11} \\
k_{21} & k_{22} & \cdots & k_{2 n} \\
\vdots & \vdots & \ddots & \vdots \\
k_{n 1} & k_{n 2} & \cdots & k_{n n}
\end{array}\right] \quad \Theta=-K^{-1}=\left(\begin{array}{cccc}
\vartheta_{11} & \vartheta_{12} & \cdots & \vartheta_{1 n} \\
\vartheta_{21} & \vartheta_{22} & \cdots & \vartheta_{2 n} \\
\vdots & \vdots & \ddots & \vdots \\
\vartheta_{n 1} & \vartheta_{n 2} & \cdots & \vartheta_{n n}
\end{array}\right)
$$

$\qquad$
$\qquad$

Theta, the negative of the inverse of the compartmental
$\qquad$ matrix, is called the mean residence time matrix. $\qquad$

## Parameters Based Upon The Compartmental Matrix

Generalization of Mean Residence Time

$\vartheta_{\mathrm{ij}} \quad$| The average time the drug entering compartment j |
| :--- |
| for the first time spends in compartment i before |
| leaving the system. |


$\frac{\vartheta_{\mathrm{ij}}}{\vartheta_{\mathrm{ii}}}, \quad \mathrm{i} \neq \mathrm{j} \quad$| The probability that a drug particle in |
| :--- |
| compartment j will eventually pass through |
| compartment i before leaving the system. |

## Compartmental Models:

 Advantages> Can handle nonlinearities
> Provide hypotheses about system structure
> Can aid in experimental design, for example to design dosing regimens
> Can support translational research

## Bias That Can Be Introduced By Noncompartmental Analysis

> Not a single sink
= Clearance rate
$\downarrow$ Mean residence time
$\downarrow$ Volume of distribution
$\uparrow$ Fractional clearance
> Not a single sink / not a single source
$\qquad$
$\downarrow$ Clearance rate
$\downarrow$ Mean residence time
$\downarrow$ Volume of distribution
$\uparrow$ Fractional clearance
JJ DiStefano III.
Noncompartmental vs compartmental analysis: some bases for choice.
Am J. Physiol. 1982;243:R1-R6

## Nonlinear Pharmacokinetics

> Example: antibody pharmacokinetics
> Often, antibodies exhibit target-mediated disposition, and thus their elimination may occur at sites remote from plasma due to binding and internalization processes $\qquad$
> This is one of many possible biological processes causing nonlinear (capacity- $\qquad$ limited) pharmacokinetic behaviors

## Impact of Noncompartmental Analysis Assumptions

When drug elimination is influenced by binding to its pharmacological target, the assumptions of noncompartmental analysis may not be met to a varying degree and parameter estimates may be misleading
> Noncompartmental analysis always requires linearity and time invariance, but it can be useful to explore nonlinearities

## Example of Dose Nonlinearities



PK example from Sheremata et al. (1999)as reported in Mager (2006)
Target-mediated drug disposition and dynamics
Biochemical Pharmacology 72(2006) 1-10


## Take Home Message

> To estimate traditional pharmacokinetic parameters, either model is probably adequate when the sampling schedule is dense, provided all assumptions required for noncompartmental analysis are met
> Sparse sampling schedule and nonlinearities may be an issue for noncompartmental analysis
$>$ Noncompartmental models are not predictive
$>$ Best strategy is probably a blend: but, careful about assumptions!

## Selected References

$\qquad$
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